<110> Goodman, Corey
      Kid, Thomas
      Brose, Katja
      Tessier-Lavigne, Marc

<120> Modulating Robo: Ligand Interactions

<130> B98-031-3

<140>
<141>

<150> 60/065,544
<151> 1997-11-14

<150> 60/081,057
<151> 1998-04-07

<160> 14

<170> PatentIn Ver. 2.0

<210> 1
<211> 4758
<212> DNA
<213> human

<220>
<221> CDS
<222> (1)..(4575)

<400> 1

```
atg cgc ggc gtt ggc tgg cag atg ctg tcc ctg tcg ctg ggg tta gtg      48
Met Arg Gly Val Gly Trp Gln Met Leu Ser Leu Ser Leu Gly Leu Val
  1               5                  10                  15

ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc      96
Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys
             20                  25                  30

tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc     144
Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
         35                  40                  45

gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga     192
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
     50                  55                  60

aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat     240
Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
 65                  70                  75                  80

cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga     288
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
                 85                  90                  95

gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga     336
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
            100                 105                 110

aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag     384
Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
            115                 120                 125

cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg     432
Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
```

```
aaa gct ttc cgt ggg gca gtt gac ata aaa aat ttg caa ctg gat tac   480
Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
145                 150                 155                 160

aac cag atc agc tgt att gaa gat ggg gca ttc agg gct ctc cgg gac   528
Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
                165                 170                 175

ctg gaa gtg ctc act ctc aac aat aac aac att act aga ctt tct gtg   576
Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
                180                 185                 190

gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca   624
Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
                195                 200                 205

aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt   672
Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
            210                 215                 220

cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc   720
Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
225                 230                 235                 240

cac ctg aga ggc cat aat gta gcc gag gtt caa aaa cga gaa ttt gtc   768
His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
                245                 250                 255

tgc agt gat gag gaa gaa ggt cac cag tca ttt atg gct cct tct tgt   816
Cys Ser Asp Glu Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys
                260                 265                 270

agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta   864
Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val
                275                 280                 285

gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag   912
Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu
                290                 295                 300

acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct   960
Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro
305                 310                 315                 320

cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc   1008
Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser
                325                 330                 335

aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc   1056
Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg

            340                 345                 350

tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc   1104
Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
                355                 360                 365

aaa agt tta ttt gaa gga ctg ttt tcc tta cag ctc cta tta ttg aat   1152
Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Leu Asn
                370                 375                 380

gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac   1200
Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His
385                 390                 395                 400

aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc   1248
Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
```

```
aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc   1296
Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
        420             425             430

cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat   1344
Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
        435             440             445

ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc   1392
Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
        450             455             460

cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc   1440
Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
465             470             475             480

cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc   1488
Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
                485             490             495

ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca   1536
Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
        500             505             510

gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc   1584
Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro
        515             520             525

cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg   1632
Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu
        530             535             540

gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac   1680
Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn
545             550             555             560

ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga   1728
Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly
                565             570             575

gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat   1776
Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn

        580             585             590

gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg   1824
Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met
        595             600             605

ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga   1872
Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly
        610             615             620

ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca   1920
Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr
625             630             635             640

gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac   1968
Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn
        645             650             655

ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga   2016
Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly
        660             665             670

gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa   2064
Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln
```

3

```
                  675                    680                    685
aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag   2112
Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln
    690                 695                 700

gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt   2160
Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu
705                 710                 715                 720

tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt   2208
Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys
                725                 730                 735

agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc   2256
Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val
                740                 745                 750

aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa   2304
Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu
            755                 760                 765

ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga   2352
Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg
        770                 775                 780

ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc   2400
Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu
785                 790                 795                 800

acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc   2448
Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr
                805                 810                 815

ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac   2496
Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp

            820                 825                 830
att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca   2544
Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser
                835                 840                 845

cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag   2592
His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln
        850                 855                 860

tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct   2640
Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala
865                 870                 875                 880

cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act   2688
Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr
                885                 890                 895

ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta   2736
Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu
            900                 905                 910

gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca   2784
Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr
        915                 920                 925

tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt   2832
Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly
        930                 935                 940

ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac   2880
Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn
```

```
cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat   2928
Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp
                965                         970                 975

gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa   2976
Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu
            980                     985                     990

gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca   3024
Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr
        995                 1000                1005

tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat   3072
Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr
    1010                1015                1020

aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg   3120
Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu
1025                1030                1035                1040

aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc   3168
Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe
                1045                1050                1055

aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat   3216
Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp

        1060                1065                1070

ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca   3264
Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr
        1075                1080                1085

gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc   3312
Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly
    1090                1095                1100

ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc   3360
Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro
1105                1110                1115                1120

tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata   3408
Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile
            1125                1130                1135

aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt   3456
Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys
            1140                1145                1150

gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag   3504
Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln
            1155                1160                1165

att cct tca gcc aag gtt cgg cct cag acg aac ata aca ctt cag att   3552
Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile
    1170                1175                1180

gcc aca gat gaa gac agc gga atc ctc ctg tat aag ggt gac aaa gac   3600
Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp
1185                1190                1195                1200

cat atc gcg gta gaa ctc tat cgg ggg cgt gtt cgt gcc agc tat gac   3648
His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg Ala Ser Tyr Asp
            1205                1210                1215

acc ggc tct cat cca gct tct gcc att tac agt gtg gag aca atc aat   3696
Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn
```

```
gat gga aac ttc cac att gtg gaa cta ctt gcc ttg gat cag agt ctc   3744
Asp Gly Asn Phe His Ile Val Glu Leu Leu Ala Leu Asp Gln Ser Leu
        1235                1240                1245

tct ttg tcc gtg gat ggt ggg aac ccc aaa atc atc act aac ttg tca   3792
Ser Leu Ser Val Asp Gly Gly Asn Pro Lys Ile Ile Thr Asn Leu Ser
    1250                1255                1260

aag cag tcc act ctg aat ttt gac tct cca ctc tat gta gga ggc atg   3840
Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met
1265                1270                1275                1280

cca ggg aag agt aac gtg gca tct ctg cgc cag gcc cct ggg cag aac   3888
Pro Gly Lys Ser Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn
                1285                1290                1295

gga acc agc ttc cac ggc tgc atc cgg aac ctt tac atc aac agt gag   3936
Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu

        1300                1305                1310

ctg cag gac ttc cag aag gtg ccg atg caa aca ggc att ttg cct ggc   3984
Leu Gln Asp Phe Gln Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly
        1315                1320                1325

tgt gag cca tgc cac aag aag gtg tgt gcc cat ggc aca tgc cag ccc   4032
Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro
    1330                1335                1340

agc agc cag gca ggc ttc acc tgc gag tgc cag gaa gga tgg atg ggg   4080
Ser Ser Gln Ala Gly Phe Thr Cys Glu Cys Gln Glu Gly Trp Met Gly
1345                1350                1355                1360

ccc ctc tgt gac caa cgg acc aat gac cct tgc ctt gga aat aaa tgc   4128
Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys
                1365                1370                1375

gta cat ggc acc tgc ttg ccc atc aat gcg ttc tcc tac agc tgt aag   4176
Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys
                1380                1385                1390

tgc ttg gag ggc cat gga ggt gtc ctc tgt gat gaa gag gag gat ctg   4224
Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu
        1395                1400                1405

ttt aac cca tgc cag gcg atc aag tgc aag cat ggg aag tgc agg ctt   4272
Phe Asn Pro Cys Gln Ala Ile Lys Cys Lys His Gly Lys Cys Arg Leu
        1410                1415                1420

tca ggt ctg ggg cag ccc tac tgt gaa tgc agc agt gga tac acg ggg   4320
Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser Gly Tyr Thr Gly
1425                1430                1435                1440

gac agc tgt gat cga gaa atc tct tgt cga ggg gaa agg ata aga gat   4368
Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp
                1445                1450                1455

tat tac caa aag cag cag ggc tat gct gct tgc caa aca acc aag aag   4416
Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln Thr Thr Lys Lys
                1460                1465                1470

gtg tcc cga tta gag tgc aga ggt ggg tgt gca gga ggg cag tgc tgt   4464
Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly Gly Gln Cys Cys
        1475                1480                1485

gga ccg ctg agg agc aag cgg cgg aaa tac tct ttc gaa tgc act gac   4512
Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe Glu Cys Thr Asp
```

6

```
ggc tcc tcc ttt gtg gac gag gtt gag aaa gtg gtg aag tgc ggc tgt   4560
Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val Lys Cys Gly Cys
1505                1510            ·         1515                1520

acg agg tgt gtg tcc taaacacact cccggcagct ctgtctttgg aaaaggttgt   4615
Thr Arg Cys Val Ser
                1525

atacttcttg accatgtggg actaatgaat gcttcatagt ggaaatattt gaaatatatt   4675


gtaaaataca gaacagactt atttttatta tgagaataaa gacttttttt ctgcatttgg   4735

aaaaaaaaaa aaaaaaact cga                                            4758
```

<210> 2
<211> 1525
<212> PRT
<213> human

<400> 2

```
Met Arg Gly Val Gly Trp Gln Met Leu Ser Leu Ser Leu Gly Leu Val
 1               5                  10                  15

Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys
            20                  25                  30

Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
            35                  40                  45

Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
     50                  55                  60

Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
 65                  70                  75                  80

Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
                85                  90                  95

Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
            100                 105                 110

Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
            115                 120                 125

Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
    130                 135                 140

Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
145                 150                 155                 160

Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
                165                 170                 175

Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
            180                 185                 190

Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
            195                 200                 205

Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
    210                 215                 220

Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
225                 230                 235                 240
```

His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
              245   250   255

Cys Ser Asp Glu Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys
          260   265   270

Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val
          275   280   285

Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu
    290   295   300

Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro
305   310   315   320

Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser
              325   330   335

Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg
              340   345   350

Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
              355   360   365

Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Leu Asn
    370   375   380

Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His
385   390   395   400

Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
              405   410   415

Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
              420   425   430

Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
              435   440   445

Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
    450   455   460

Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
465   470   475   480

Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
              485   490   495

Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
              500   505   510

Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro
              515   520   525

Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu
    530   535   540

Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn
545   550   555   560

Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly
              565   570   575

Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn
          580   585   590

Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met

8

Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly
    610   615   .   620

Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr
625   630   635   640

Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn
            645   650   655

Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly
            660   665   670

Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln
        675   680   685

Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln
    690   695   700

Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu
705   710   715   720

Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys
            725   730   735

Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val
        740   745   750

Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu
        755   760   765

Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg
    770   775   780

Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu
785   790   795   800

Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr
            805   810   815

Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp
        820   825   830

Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser
        835   840   845

His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln
850   855   860

Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala
865   870   875   880

Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr

Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu

        900   905   910

Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr
    915   920   925

Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly
930   935   940

Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn
945   950   955   960

Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp

Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu
    980   985   990

Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr
    995   1000   1005

Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr
  1010   1015   1020

Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu
1025   1030   1035   1040

Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe
    1045   1050   1055

Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp
    1060   1065   1070

Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr
   1075   1080   1085

Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly
  1090   1095   1100

Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro
1105   1110   1115   1120

Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile
    1125   1130   1135

Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys
    1140   1145   1150

Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln
   1155   1160   1165

Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile
  1170   1175   1180

Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp
1185   1190   1195   1200

His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg Ala Ser Tyr Asp
    1205   1210   1215

Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn

     1220   1225   1230

Asp Gly Asn Phe His Ile Val Glu Leu Leu Ala Leu Asp Gln Ser Leu
   1235   1240   1245

Ser Leu Ser Val Asp Gly Gly Asn Pro Lys Ile Ile Thr Asn Leu Ser
  1250   1255   1260

Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met
1265   1270   1275   1280

Pro Gly Lys Ser Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn
    1285   1290   1295

Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu
   1300   1305   1310

Leu Gln Asp Phe Gln Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly
   1315   1320   1325

Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro
    1330   1335   1340

Ser Ser Gln Ala Gly Phe Thr Cys Glu Cys Gln Glu Gly Trp Met Gly
1345   1350   1355   1360

Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys
                1365   1370   1375

Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys
            1380   1385   1390

Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Asp Leu
        1395   1400   1405

Phe Asn Pro Cys Gln Ala Ile Lys Cys Lys His Gly Lys Cys Arg Leu
    1410   1415   1420

Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser Gly Tyr Thr Gly
1425   1430   1435   1440

Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp
            1445   1450   1455

Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln Thr Thr Lys Lys
            1460   1465   1470

Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly Gly Gln Cys Cys
        1475   1480   1485

Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe Glu Cys Thr Asp
    1490   1495   1500

Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val Lys Cys Gly Cys
1505   1510   1515   1520

Thr Arg Cys Val Ser
            1525

<210> 3
<211> 105
<212> PRT
<213> human

<400> 3
Ser Pro Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly
  1   5   10   15

Leu Met Glu Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg
                20   25   30

Leu Glu Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln
        35   40   45

Tyr Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
    50   55   60

Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu Val
65   70   75   80

Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe Asp Gly
                85   90   95

Leu Val Ser Leu Gln Leu Leu Leu Leu
            100   105

<210> 4
<211> 138
<212> PRT
<213> human

<400> 4
Glu Gly Ala Phe Asn Gly Ala Ala Ser Val Gln Glu Leu Met Leu Thr
1   5   10   15

Gly Asn Gln Leu Glu Thr Val His Gly Arg Gly Phe Arg Gly Gly Leu
            20   25   30

Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn Leu Ile Gly Cys Val
        35   40   45

Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser Val Arg Leu Leu Ser Leu
    50   55   60

Tyr Asp Asn Arg Ile Thr Thr Ile Thr Pro Gly Ala Phe Thr Thr Leu
65   70   75   80

Val Ser Leu Ser Thr Ile Asn Leu Leu Ser Asn Pro Phe Asn Cys Asn
            85   90   95

Cys His Leu Gly Ala Gly Leu Gly Lys Trp Leu Arg Lys Arg Arg Ile
            100   105   110

Val Ser Gly Asn Pro Arg Cys Gln Lys Pro Phe Phe Leu Lys Glu Ile
        115   120   125

Pro Ile Gln Gly Val Gly His Pro Gly Ile
    130   135

<210> 5
<211> 160
<212> PRT
<213> human

<400> 5
Trp Pro Arg Cys Glu Cys Met Pro Gly Tyr Ala Gly Asp Asn Cys Ser
1   5   10   15

Glu Asn Gln Asp Asp Cys Arg Asp His Arg Cys Gln Asn Gly Ala Gln
            20   25   30

Cys Met Asp Glu Val Asn Ser Tyr Ser Cys Leu Cys Ala Glu Gly Tyr
        35   40   45

Ser Gly Gln Leu Cys Glu Ile Pro Pro His Leu Pro Ala Pro Lys Ser
    50   55   60

Pro Cys Glu Gly Thr Glu Cys Gln Asn Gly Ala Asn Cys Val Asp Gln
65   70   75   80

Gly Asn Arg Pro Val Cys Gln Cys Leu Pro Gly Phe Gly Gly Pro Glu
            85   90   95

Cys Glu Lys Leu Leu Ser Val Asn Phe Val Asp Arg Asp Thr Tyr Leu
            100   105   110

Gln Phe Thr Asp Leu Gln Asn Trp Xaa Arg Xaa Asn Ile Thr Leu Gln
        115   120   125

Val Phe Thr Ala Glu Asp Asn Gly Ile Leu Leu Tyr Asn Gly Gly Asn
    130   135   140

Asp His Ile Ala Val Xaa Leu Tyr Xaa Gly His Val Arg Phe Ser Tyr

12

<210> 6
<211> 103
<212> PRT
<213> human

<400> 6
Gln Cys His Ile Ser Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro
 1   5   10   15

Gly Phe Ser Gly Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln
            20   25   30

Val Val Arg Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala
            35   40   45

Thr Ala Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro
        50   55   60

Gln Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
65   70   75   80

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu Glu
                85   90   95

Cys Gly Cys Leu Ala Cys Ser
                100

<210> 7
<211> 1480
<212> PRT
<213> Drosophila melanogaster

<400> 7
Met Ala Ala Pro Ser Arg Thr Thr Leu Met Pro Pro Pro Phe Arg Leu
 1   5   10   15

Gln Leu Arg Leu Leu Ile Leu Pro Ile Leu Leu Leu Arg His Asp
            20   25   30

Ala Val His Ala Glu Pro Tyr Ser Gly Gly Phe Gly Ser Ser Ala Val
            35   40   45

Ser Ser Gly Gly Leu Gly Ser Val Gly Ile His Ile Pro Gly Gly Gly
        50   55   60

Val Gly Val Ile Thr Glu Ala Arg Cys Pro Arg Val Cys Ser Cys Thr
65   70   75   80

Gly Leu Asn Val Asp Cys Ser His Arg Gly Leu Thr Ser Val Pro Arg
                85   90   95

Lys Ile Ser Ala Asp Val Glu Arg Leu Glu Leu Gln Gly Asn Asn Leu
                100   105   110

Thr Val Ile Tyr Glu Thr Asp Phe Gln Arg Leu Thr Lys Leu Arg Met
                115   120   125

Leu Gln Leu Thr Asp Asn Gln Ile His Thr Ile Glu Arg Asn Ser Phe
        130   135   140

Gln Asp Leu Val Ser Leu Glu Arg Leu Asp Ile Ser Asn Asn Val Ile

```
        145                    150                      155                      160
Thr Thr Val Gly Arg Arg Val Phe Lys Gly Ala Gln Ser Leu Arg Ser
            165              170                  175

Leu Gln Leu Asp Asn Asn Gln Ile Thr Cys Leu Asp Glu His Ala Phe
            180              185                  190

Lys Gly Leu Val Glu Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Leu
            195              200                  205

Thr Ser Leu Pro His Asn Ile Phe Gly Gly Leu Gly Arg Leu Arg Ala
            210              215                  220

Leu Arg Leu Ser Asp Asn Pro Phe Ala Cys Asp Cys His Leu Ser Trp
225                  230                  235                  240

Leu Ser Arg Phe Leu Arg Ser Ala Thr Arg Leu Ala Pro Tyr Thr Arg
                245                  250                  255

Cys Gln Ser Pro Ser Gln Leu Lys Gly Gln Asn Val Ala Asp Leu His
            260              265                  270

Asp Gln Glu Phe Lys Cys Ser Gly Leu Thr Glu His Ala Pro Met Glu
            275              280                  285

Cys Gly Ala Glu Asn Ser Cys Pro His Pro Cys Arg Cys Ala Asp Gly
    290              295                  300

Ile Val Asp Cys Arg Glu Lys Ser Leu Thr Ser Val Pro Val Thr Leu
305                  310                  315                  320

Pro Asp Asp Thr Thr Asp Val Arg Leu Glu Gln Asn Phe Ile Thr Glu
                325                  330                  335

Leu Pro Pro Lys Ser Phe Ser Ser Phe Arg Arg Leu Arg Arg Ile Asp
                340                  345                  350

Leu Ser Asn Asn Asn Ile Ser Arg Ile Ala His Asp Ala Leu Ser Gly
                355                  360                  365

Leu Lys Gln Leu Thr Thr Leu Val Leu Tyr Gly Asn Lys Ile Lys Asp
    370                  375                  380

Leu Pro Ser Gly Val Phe Lys Gly Leu Gly Ser Leu Arg Leu Leu Leu
385                  390                  395                  400

Leu Asn Ala Asn Glu Ile Ser Cys Ile Arg Lys Asp Ala Phe Arg Asp
                405                  410                  415

Leu His Ser Leu Ser Leu Leu Ser Leu Tyr Asp Asn Asn Ile Gln Ser
            420              425                  430

Leu Ala Asn Gly Thr Phe Asp Ala Met Lys Ser Met Lys Thr Val His
            435              440                  445

Leu Ala Lys Asn Pro Phe Ile Cys Asp Cys Asn Leu Arg Trp Leu Ala
    450                  455                  460

Asp Tyr Leu His Lys Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Glu
465                  470                  475                  480

Ser Pro Lys Arg Met His Arg Arg Arg Ile Glu Ser Leu Arg Glu Glu
                485                  490                  495

Lys Phe Lys Cys Ser Trp Gly Glu Leu Arg Met Lys Leu Ser Gly Glu
            500              505                  510
```

14

```
Cys Arg Met Asp Ser Asp Cys Pro Ala Met Cys His Cys Glu Gly Thr
        515             520             525

Thr Val Asp Cys Thr Gly Arg Arg Leu Lys Glu Ile Pro Arg Asp Ile
    530             535             540

Pro Leu His Thr Thr Glu Leu Leu Leu Asn Asp Asn Glu Leu Gly Arg
545             550             555             560

Ile Ser Ser Asp Gly Leu Phe Gly Arg Leu Pro His Leu Val Lys Leu
                565             570             575

Glu Leu Lys Arg Asn Gln Leu Thr Gly Ile Glu Pro Asn Ala Phe Glu
            580             585             590

Gly Ala Ser His Ile Gln Glu Leu Gln Leu Gly Glu Asn Lys Ile Lys
        595             600             605

Glu Ile Ser Asn Lys Met Phe Leu Gly Leu His Gln Leu Lys Thr Leu
    610             615             620

Asn Leu Tyr Asp Asn Gln Ile Ser Cys Val Met Pro Gly Ser Phe Glu
625             630             635             640

His Leu Asn Ser Leu Thr Ser Leu Asn Leu Ala Ser Asn Pro Phe Asn
                645             650             655

Cys Asn Cys His Leu Ala Trp Phe Ala Glu Cys Val Arg Lys Lys Ser
            660             665             670

Leu Asn Gly Gly Ala Ala Arg Cys Gly Ala Pro Ser Lys Val Arg Asp
        675             680             685

Val Gln Ile Lys Asp Leu Pro His Ser Glu Phe Lys Cys Ser Ser Glu
    690             695             700

Asn Ser Glu Gly Cys Leu Gly Asp Gly Tyr Cys Pro Pro Ser Cys Thr
705             710             715             720

Cys Thr Gly Thr Val Val Ala Cys Ser Arg Asn Gln Leu Lys Glu Ile
            725             730             735

Pro Arg Gly Ile Pro Ala Glu Thr Ser Glu Leu Tyr Leu Glu Ser Asn
        740             745             750

Glu Ile Glu Gln Ile His Tyr Glu Arg Ile Arg His Leu Arg Ser Leu
    755             760             765

Thr Arg Leu Asp Leu Ser Asn Asn Gln Ile Thr Ile Leu Ser Asn Tyr
    770             775             780

Thr Phe Ala Asn Leu Thr Lys Leu Ser Thr Leu Ile Ile Ser Tyr Asn
785             790             795             800

Lys Leu Gln Cys Leu Gln Arg His Ala Leu Ser Gly Leu Asn Asn Leu
            805             810             815

Arg Val Val Ser Leu His Gly Asn Arg Ile Ser Met Leu Pro Glu Gly
        820             825             830

Ser Phe Glu Asp Leu Lys Ser Leu Thr His Ile Ala Leu Gly Ser Asn
        835             840             845

Pro Leu Tyr Cys Asp Cys Gly Leu Lys Trp Phe Ser Asp Trp Ile Lys
    850             855             860

Leu Asp Tyr Val Glu Pro Gly Ile Ala Arg Cys Ala Glu Pro Glu Gln
865             870             875             880
```

15

Met Lys Asp Lys Leu ● Leu Ser Thr Pro Ser Ser Ser ● Val Cys
              885   890   895

Arg Gly Arg Val Arg Asn Asp Ile Leu Ala Lys Cys Asn Ala Cys Phe
          900   905   910

Glu Gln Pro Cys Gln Asn Gln Ala Gln Cys Val Ala Leu Pro Gln Arg
          915   920   925

Glu Tyr Gln Cys Leu Cys Gln Pro Gly Tyr His Gly Lys His Cys Glu
          930   935   940

Phe Met Ile Asp Ala Cys Tyr Gly Asn Pro Cys Arg Asn Asn Ala Thr
945   950   955   960

Cys Thr Val Leu Glu Glu Gly Arg Phe Ser Cys Gln Cys Ala Pro Gly
          965   970   975

Tyr Thr Gly Ala Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu Gly Glu
          980   985   990

Ile Lys Cys Gln Asn Asn Ala Thr Cys Ile Asp Gly Val Glu Ser Tyr
          995   1000   1005

Lys Cys Glu Cys Gln Pro Gly Phe Ser Gly Glu Phe Cys Asp Thr Lys
        1010   1015   1020

Ile Gln Phe Cys Ser Pro Glu Phe Asn Pro Cys Ala Asn Gly Ala Lys
1025   1030   1035   1040

Cys Met Asp His Phe Thr His Tyr Ser Cys Asp Cys Gln Ala Gly Phe
              1045   1050   1055

His Gly Thr Asn Cys Thr Asp Asn Ile Asp Asp Cys Gln Asn His Met
              1060   1065   1070

Cys Gln Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Asp Tyr Gln Cys
        1075   1080   1085

Arg Cys Pro Asp Asp Tyr Thr Gly Lys Tyr Cys Glu Gly His Asn Met
        1090   1095   1100

Ile Ser Met Met Tyr Pro Gln Thr Ser Pro Cys Gln Asn His Glu Cys
1105   1110   1115   1120

Lys His Gly Val Cys Phe Gln Pro Asn Ala Gln Gly Ser Asp Tyr Leu
              1125   1130   1135

Cys Arg Cys His Pro Gly Tyr Thr Gly Lys Trp Cys Glu Tyr Leu Thr
        1140   1145   1150

Ser Ile Ser Phe Val His Asn Asn Ser Phe Val Glu Leu Glu Pro Leu
        1155   1160   1165

Arg Thr Arg Pro Glu Ala Asn Val Thr Ile Val Phe Ser Ser Ala Glu
        1170   1175   1180

Gln Asn Gly Ile Leu Met Tyr Asp Gly Gln Asp Ala His Leu Ala Val
1185   1190   1195   1200

Glu Leu Phe Asn Gly Arg Ile Arg Val Ser Tyr Asp Val Gly Asn His
              1205   1210   1215

Pro Val Ser Thr Met Tyr Ser Phe Glu Met Val Ala Asp Gly Lys Tyr
              1220   1225   1230

His Ala Val Glu Leu Leu Ala Ile Lys Lys Asn Phe Thr Leu Arg Val
        1235   1240   1245

Asp Arg Gly Leu Ala Arg Ser Ile Ile Asn Glu Gly Ser Asn Asp Tyr
        1250   1255   1260

Leu Lys Leu Thr Thr Pro Met Phe Leu Gly Gly Leu Pro Val Asp Pro
1265   1270   1275   1280

Ala Gln Gln Ala Tyr Lys Asn Trp Gln Ile Arg Asn Leu Thr Ser Phe
                1285   1290   1295

Lys Gly Cys Met Lys Glu Val Trp Ile Asn His Lys Leu Val Asp Phe
            1300   1305   1310

Gly Asn Ala Gln Arg Gln Gln Lys Ile Thr Pro Gly Cys Ala Leu Leu
            1315   1320   1325

Glu Gly Glu Gln Gln Glu Glu Glu Asp Asp Glu Gln Asp Phe Met Asp
        1330   1335   1340

Glu Thr Pro His Ile Lys Glu Glu Pro Val Asp Pro Cys Leu Glu Asn
1345   1350   1355   1360

Lys Cys Arg Arg Gly Ser Arg Cys Val Pro Asn Ser Asn Ala Arg Asp
                1365   1370   1375

Gly Tyr Gln Cys Lys Cys Lys His Gly Gln Arg Gly Arg Tyr Cys Asp
            1380   1385   1390

Gln Gly Glu Gly Ser Thr Glu Pro Pro Thr Val Thr Ala Ala Ser Thr
        1395   1400   1405

Cys Arg Lys Glu Gln Val Arg Glu Tyr Tyr Thr Glu Asn Asp Cys Arg
    1410   1415   1420

Ser Arg Gln Pro Leu Lys Tyr Ala Lys Cys Val Gly Gly Cys Gly Asn
1425   1430   1435   1440

Gln Cys Cys Ala Ala Lys Ile Val Arg Arg Arg Lys Val Arg Met Val
                1445   1450   1455

Cys Ser Asn Asn Arg Lys Tyr Ile Lys Asn Leu Asp Ile Val Arg Lys
                1460   1465   1470

Cys Gly Cys Thr Lys Lys Cys Tyr
        1475   1480

<210> 8
<211> 155
<212> PRT
<213> Caenorhabditis elegans

<400> 8
Arg Asn Pro Xaa Ile Cys Asp Cys Asn Leu Gln Trp Leu Ala Gln Ile
  1   5   10   15

Asn Leu Gln Lys Asn Ile Glu Thr Ser Gly Ala Arg Cys Glu Gln Pro
            20   25   30

Lys Arg Leu Arg Lys Lys Lys Phe Ala Thr Leu Pro Pro Asn Lys Phe
        35   40   45

Lys Cys Lys Gly Ser Glu Ser Phe Val Ser Met Tyr Ala Asp Ser Cys
    50   55   60

Phe Ile Asp Ser Ile Cys Pro Thr Gln Cys Asp Cys Tyr Gly Thr Thr

Val Asp Cys Asn Lys Arg Gly Leu Asn Thr Ile Pro Thr Ser Ile Pro
            85   90   95

Arg Phe Ala Thr Gln Leu Leu Leu Ser Gly Asn Asn Ile Ser Thr Val
            100   105   110

Asp Leu Asn Ser Asn Ile His Val Leu Glu Asn Leu Glu Xaa Leu Asp
            115   120   125

Leu Ser Asn Asn His Ile Thr Phe Ile Asn Asp Lys Ser Phe Glu Lys
145   150   155

Leu Ser Lys Leu Arg Glu Leu Xaa Leu Asn Asp
145   150   155

<210> 9
<211> 735
<212> PRT
<213> Caenorhabditis elegans

<400> 9
Ser Asn Lys Asn Leu Thr Ser Phe Pro Ser Arg Ile Pro Phe Asp Thr
  1   5   10   15

Thr Glu Leu Tyr Leu Asp Ala Asn Tyr Ile Asn Glu Ile Pro Ala His
            20   25   30

Asp Leu Asn Arg Leu Tyr Ser Leu Thr Lys Leu Asp Leu Ser His Asn
            35   40   45

Arg Leu Ile Ser Leu Glu Asn Asn Thr Phe Ser Asn Leu Thr Arg Leu
    50   55   60

Ser Thr Leu Ile Ile Ser Tyr Asn Lys Leu Arg Cys Leu Gln Pro Leu
65   70   75   80

Ala Phe Asn Gly Leu Asn Ala Leu Arg Ile Leu Ser Leu His Gly Asn
            85   90   95

Asp Ile Ser Phe Leu Pro Gln Ser Ala Phe Ser Asn Leu Thr Ser Ile
            100   105   110

Thr His Ile Ala Val Gly Ser Asn Ser Leu Tyr Cys Asp Cys Asn Met
            115   120   125

Ala Trp Phe Ser Lys Trp Ile Lys Ser Lys Phe Ile Glu Ala Gly Ile
    130   135   140

Ala Arg Cys Glu Tyr Pro Asn Thr Val Ser Asn Gln Leu Leu Leu Thr
145   150   155   160

Ala Gln Pro Tyr Gln Phe Thr Cys Asp Ser Lys Val Pro Thr Lys Leu
            165   170   175

Ala Thr Lys Cys Asp Leu Cys Leu Asn Ser Pro Cys Lys Asn Asn Ala
            180   185   190

Ile Cys Glu Thr Thr Ser Ser Arg Lys Tyr Thr Cys Asn Cys Thr Pro
    195   200   205

Gly Phe Tyr Gly Val His Cys Glu Asn Gln Ile Asp Ala Cys Tyr Gly
    210   215   220

Ser Pro Cys Leu Asn Asn Ala Thr Cys Lys Val Ala Gln Ala Gly Arg
225   230   235   240

Phe Asn Cys Tyr Cys Asn Lys Gly Phe Glu Gly Asp Tyr Cys Glu Lys
                245   250   255

Asn Ile Asp Asp Cys Val Asn Ser Lys Cys Glu Asn Gly Gly Lys Cys
            260   265   270

Val Asp Leu Val Arg Phe Cys Ser Glu Glu Leu Lys Asn Phe Gln Ser
            275   280   285

Phe Gln Ile Asn Ser Tyr Arg Cys Asp Cys Pro Met Glu Tyr Glu Gly
    290   295   300

Lys His Cys Glu Asp Lys Leu Glu Tyr Cys Thr Lys Lys Leu Asn Pro
305   310   315   320

Cys Glu Asn Asn Gly Lys Cys Ile Pro Ile Asn Gly Ser Tyr Ser Cys
                325   330   335

Met Cys Ser Pro Gly Phe Thr Gly Asn Asn Cys Glu Thr Asn Ile Asp
            340   345   350

Asp Cys Lys Asn Val Glu Cys Gln Asn Gly Gly Ser Cys Val Asp Gly
        355   360   365

Ile Leu Ser Tyr Asp Cys Leu Cys Arg Pro Gly Tyr Ala Gly Gln Tyr
    370   375   380

Cys Glu Ile Pro Pro Met Met Asp Met Glu Tyr Gln Lys Thr Asp Ala
385   390   395   400

Cys Gln Gln Ser Ala Cys Gly Gln Gly Glu Cys Val Ala Ser Gln Asn
                405   410   415

Ser Ser Asp Phe Thr Cys Lys Cys His Glu Gly Phe Ser Gly Pro Ser
            420   425   430

Cys Asp Arg Gln Met Ser Val Gly Phe Lys Asn Pro Gly Ala Tyr Leu
            435   440   445

Ala Leu Asp Pro Leu Ala Ser Asp Gly Thr Ile Thr Met Thr Leu Arg
    450   455   460

Thr Thr Ser Lys Ile Gly Ile Leu Leu Tyr Tyr Gly Asp Asp His Phe
465   470   475   480

Val Ser Ala Glu Leu Tyr Asp Gly Arg Val Lys Leu Val Tyr Tyr Ile
            485   490   495

Gly Asn Phe Pro Ala Ser His Met Tyr Ser Ser Val Lys Val Asn Asp
            500   505   510

Gly Leu Pro His Arg Ile Ser Ile Arg Thr Ser Glu Arg Lys Cys Phe
        515   520   525

Leu Gln Ile Asp Lys Asn Pro Val Gln Ile Val Glu Asn Ser Gly Lys
    530   535   540

Ser Asp Gln Leu Ile Thr Lys Gly Lys Glu Met Leu Tyr Ile Gly Gly
545   550   555   560

Leu Pro Ile Glu Lys Ser Gln Asp Ala Lys Arg Arg Phe His Val Lys
                565   570   575

Asn Ser Glu Ser Leu Lys Gly Cys Ile Ser Ser Ile Thr Ile Asn Glu
            580   585   590

Val Pro Ile Asn Leu Gln Gln Ala Leu Glu Asn Val Asn Thr Glu Gln

```
                595                          600                          605
    Ser Cys Ser Ala Thr Val Asn Phe Cys Ala Gly Ile Asp Cys Gly Asn
        610                     615                 620

    Gly Lys Cys Thr Asn Asn Ala Leu Ser Pro Lys Gly Tyr Met Cys Gln
    625                     630                 635                 640

    Cys Asp Ser His Phe Ser Gly Glu His Cys Asp Glu Lys Arg Ile Lys
                    645                 650                 655

    Cys Asp Lys Gln Lys Phe Arg Arg His His Ile Glu Asn Glu Cys Arg
                660                 665                 670

    Ser Val Asp Arg Ile Lys Ile Ala Glu Cys Asn Gly Tyr Cys Gly Gly
                675                 680                 685

    Glu Gln Asn Cys Cys Thr Ala Val Lys Lys Lys Gln Arg Lys Val Lys
            690                 695                 700

    Met Ile Cys Lys Asn Gly Thr Thr Lys Ile Ser Thr Val His Ile Ile
    705                     710                 715                 720

    Arg Gln Cys Gln Cys Glu Pro Thr Lys Ser Val Leu Ser Glu Lys
                    725                 730                 735


    <210> 10
    <211> 154

    <212> PRT
    <213> mouse

    <400> 10
    Asp Pro Leu Pro Val His His Arg Cys Glu Cys Met Leu Gly Tyr Thr
    1               5                   10                  15

    Gly Asp Asn Cys Ser Glu Asn Gln Asp Asp Cys Lys Asp His Lys Cys
                20                  25                  30

    Gln Asn Gly Ala Gln Cys Val Asp Glu Val Asn Ser Tyr Ala Cys Leu
            35                  40                  45

    Cys Val Glu Gly Tyr Ser Gly Gln Leu Cys Glu Ile Pro Pro Ala Pro
        50                  55                  60

    Arg Ser Ser Cys Glu Gly Thr Glu Cys Gln Asn Gly Ala Asn Cys Val
    65                  70                  75                  80

    Asp Gln Gly Ser Arg Pro Val Cys Gln Cys Leu Pro Gly Phe Gly Gly
                    85                  90                  95

    Pro Glu Cys Glu Lys Leu Leu Ser Val Asn Phe Val Asp Arg Asp Thr
                100                 105                 110

    Tyr Leu Gln Phe Thr Asp Leu Gln Asn Trp Pro Arg Ala Asn Ile Thr
            115                 120                 125

    Leu Gln Val Ser Thr Ala Glu Asp Asn Gly Ile Leu Leu Tyr Asn Gly
        130                 135                 140

    Asp Asn Asp His Ile Ala Val Glu Leu Tyr
    145                 150


    <210> 11
    <211> 110
    <212> PRT
    <213> mouse
```

20

<400> 11
```
Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser Asp Arg Gly Glu
1               5               10              15

Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His His Cys Glu Gln
            20              25              30

Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala Ile Arg Arg Gln
        35              40              45

Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val Pro Ile Met Glu
    50              55              60

Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro Ile Arg Ser Lys
65              70              75              80

Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser Ser Phe Val Glu
            85              90              95

Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala Cys Ser
            100             105             110
```

<210> 12
<211> 134
<212> PRT
<213> mouse

<400> 12
```
His Leu Arg Val Leu Gln Leu Met Glu Asn Arg Ile Ser Thr Ile Glu
1               5               10              15

Arg Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn
            20              25              30

Arg Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala
        35              40              45

Arg Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro
    50              55              60

Arg Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp
65              70              75              80

Tyr Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg
            85              90              95

Asp Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser
            100             105             110

Val Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His
            115             120             125

Ser Asn Asn Leu Tyr Cys
    130
```

<210> 13
<211> 104
<212> PRT
<213> mouse

<400> 13
```
Asn Asn Asp Asp Cys Val Gly His Lys Cys Arg His Gly Ala Gln Cys
1               5               10              15

Val Asp Glu Val Asn Gly Tyr Thr Cys Ile Cys Pro Gln Gly Phe Ser
```

```
Gly Leu Phe Cys Glu His Pro Pro Met Val Leu Leu Gln Thr Ser
          35                    40                    45

Pro Cys Asp Gln Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val
          50                    55                    60

Gln Gln Glu Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg
     65                    70                    75                80

Cys Glu Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val
                    85                    90                    95


Glu Leu Ala Ser Ala Lys Val Arg
                    100
```
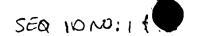
<210> 14
<211> 243
<212> PRT
<213> mouse

<400> 14
```
Ile Leu Asp Val Ala Ser Leu Arg Gln Ala Pro Gly Glu Asn Gly Thr
 1               5                    10                    15

Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu Leu Gln
               20                    25                    30

Asp Phe Arg Lys Met Pro Met Gln Thr Gly Ile Leu Pro Gly Cys Glu
          35                    40                    45

Pro Cys His Lys Lys Val Cys Ala His Gly Cys Cys Gln Pro Ser Ser
          50                    55                    60

Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu Gly Trp Met Gly Pro Leu
     65                    70                    75                80

Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys Val His
                    85                    90                    95

Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys Cys Leu
               100                   105                   110

Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe Asn
          115                   120                   125

Pro Cys Gln Met Ile Lys Cys Lys His Gly Lys Cys Arg Leu Ser Gly
     130                   135                   140

Val Gly Gln Pro Tyr Cys Glu Cys Asn Ser Gly Phe Thr Gly Asp Ser
145                   150                   155                   160

Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp Tyr Tyr
               165                   170                   175

Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln Thr Thr Lys Lys Val Ser
          180                   185                   190

Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly Gly Gln Cys Cys Gly Pro
          195                   200                   205

Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe Glu Cys Thr Asp Gly Ser
     210                   215                   220

Ser Phe Val Asp Glu Val Glu Lys Val Val Lys Cys Gly Cys Ala Arg
225                   230                   235                   240
```

Cys Ala Ser

Sequence of Human Slit-1

DNA sequence and predicted protein product. Base pair and amino acid
number are indicated on the right hand side.

```
ATGCGCGGCGTTGGCTGGCAGATGCTGTCCCTGTCGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCG   75
 M  R  G  V  G  W  Q  M  L  S  L  S  L  G  L  V  L  A  I  L  N  K  V  A  P      25

CAGGCGTGCCCGGCGCAGTGCTCTTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGTGCCC   150
 Q  A  C  P  A  Q  C  S  C  S  G  S  T  V  D  C  H  G  L  A  L  R  S  V  P      50

AGGAATATCCCCCGCAACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGAAGACAGATTTT   225
 R  N  I  P  R  N  T  E  R  L  D  L  N  G  N  N  I  T  R  I  T  K  T  D  F      75

GCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAAGAGGAGCATTCCAG   300
 A  G  L  R  H  L  R  V  L  Q  L  M  E  N  K  I  S  T  I  E  R  G  A  F  Q     100

GATCTTAAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCCTGAGTTGCTGTTTCTTGGG   375
 D  L  K  E  L  E  R  L  R  L  N  R  N  H  L  Q  L  F  P  E  L  L  F  L  G     125

ACTGCGAAGCTATACAGGCTTGATCTCAGTGAAAACCAAATTCAGGCAATCCCAAGGAAGCTTTCCGTGGGGCA   450
 T  A  K  L  Y  R  L  D  L  S  E  N  Q  I  Q  A  I  P  R  K  A  F  R  G  A     150

GTTGACATAAAAAATTTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTCAGGGCTCTCCGG   525
 V  D  I  K  N  L  Q  L  D  Y  N  Q  I  S  C  I  E  D  G  A  F  R  A  L  R     175

GACCTGGAAGTGCTCACTCTCAACAATAACAACATTACTAGACTTTCTGTGGCAAGTTTCAACCATATGCCTAAA   600
 D  L  E  V  L  T  L  N  N  N  N  I  T  R  L  S  V  A  S  F  N  H  M  P  K     200

CTTAGGACTTTTCGACTGCATTCAAACAACCTGTATTGTGACTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGC   675
 L  R  T  F  R  L  H  S  N  N  L  Y  C  D  C  H  L  A  W  L  S  D  W  L  R     225

AAAAGGCCTCGGGTTGGTCTGTACACTCAGTGTATGGGCCCCTCCCACCTGAGAGGCCATAATGTAGCCGAGGTT   750
 K  R  P  R  V  G  L  Y  T  Q  C  M  G  P  S  H  L  R  G  H  N  V  A  E  V     250

CAAAAACGAGAATTTGTCTGCAGTGATGAGGAAGAAGGTCACCAGTCATTTATGGCTCCTTCTTGTAGTGTTTTG   825
 Q  K  R  E  F  V  C  S  D  E  E  G  H  Q  S  F  M  A  P  S  C  S  V  L     275

CACTGCCCTGCCGCCTGTACCTGTAGCAACAATATCGTAGACTGTCGTGGGAAAGGTCTCACTGAGATCCCCACA   900
 H  C  P  A  A  C  T  C  S  N  N  I  V  D  C  R  G  K  G  L  T  E  I  P  T     300

AATCTTCCAGAGACCATCACAGAAATACGTTTGGAACAGAACACAATCAAAGTCATCCCTCCTGGAGCTTTCTCA   975
 N  L  P  E  T  I  T  E  I  R  L  E  Q  N  T  I  K  V  I  P  P  G  A  F  S     325

CCATATAAAAAGCTTAGACGAATTGACCTGAGCAATAATCAGATCTCTGAACTTGCACCAGATGCTTTCCAAGGA   1050
 P  Y  K  K  L  R  R  I  D  L  S  N  N  Q  I  S  E  L  A  P  D  A  F  Q  G     350

CTACGCTCTCTGAATTCACTTGTCCTCTATGGAAATAAAATCACAGAACTCCCCAAAAGTTTATTTGAAGGACTG   1125
 L  R  S  L  N  S  L  V  L  Y  G  N  K  I  T  E  L  P  K  S  L  F  E  G  L     375

TTTTCCTTACAGCTCCTATTATTGAATGCCAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCAC   1200
 F  S  L  Q  L  L  L  N  A  N  K  I  N  C  L  R  V  D  A  F  Q  D  L  H     400

AACTTGAACCTTCTCTCCCTATATGACAACAAGCTTCAGACCATCGCCAAGGGGACCTTTTCACCTCTTCGGGCC   1275
 N  L  N  L  L  S  L  Y  D  N  K  L  Q  T  I  A  K  G  T  F  S  P  L  R  A     425

ATTCAAACTATGCATTTGGCCCAGAACCCCTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCCAT   1350
 I  Q  T  M  H  L  A  Q  N  P  F  I  C  D  C  H  L  K  W  L  A  D  Y  L  H     450

ACCAACCCGATTGAGACCAGTGGTGCCCGTTGCACCAGCCCCCGCCGCCTGGCAAACAAAAGAATTGGACAGATC   1425
 T  N  P  I  E  T  S  G  A  R  C  T  S  P  R  R  L  A  N  K  R  I  G  Q  I     475

AAAAGCAAGAAATTCCGTTGTTCAGGTACAGAAGATTATCGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTG   1500
 K  S  K  K  F  R  C  S  G  T  E  D  Y  R  S  K  L  S  G  D  C  F  A  D  L     500
```

```
GCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCACAGTAGATTGCTCTAATCAAAAGCTCAACAAAATCCCGGAG   1575
 A   C   P   E   K   C   R   C   E   G   T   T   V   D   C   S   N   Q   K   L   N   K   I   P   E    525

CACATTCCCCAGTACACTGCAGAGTTGCGTCTCAATAATAATGAATTTACCGTGTTGGAAGCCACAGGAATCTTT   1650
 H   I   P   Q   Y   T   A   E   L   R   L   N   N   N   E   F   T   V   L   E   A   T   G   I   F    550

AAGAAACTTCCTCAATTACGTAAAATAAAACTTTAGCAACAATAAGATCACAGATATTGAGGAGGGAGCATTTGAA   1725
 K   K   L   P   Q   L   R   K   I   N   F   S   N   N   K   I   T   D   I   E   E   G   A   F   E    575

GGAGCATCTGGTGTAAATGAAATACTTCTTACGAGTAATCGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGA   1800
 G   A   S   G   V   N   E   I   L   L   T   S   N   R   L   E   N   V   Q   H   K   M   F   K   G    600

TTGGAAAGCCTCAAAACTTTGATGTTGAGAAGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTC   1875
 L   E   S   L   K   T   L   M   L   R   S   N   R   I   T   C   V   G   N   D   S   F   I   G   L    625

AGTTCTGTGCGTTTGCTTTCTTTGTATGATAATCAAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCAT   1950
 S   S   V   R   L   L   S   L   Y   D   N   Q   I   T   T   V   A   P   G   A   F   D   T   L   H    650

TCTTTATCTACTCTAAACCTCTTGGCCAATCCTTTTAACTGTAACTGCTACCTGGCTTGGTTGGGAGAGTGGCTG   2025
 S   L   S   T   L   N   L   L   A   N   P   F   N   C   N   C   Y   L   A   W   L   G   E   W   L    675

AGAAAGAAGAGAATTGTCACGGGAAATCCTAGATGTCAAAAACCATACTTCCTGAAAGAAATACCCATCCAGGAT   2100
 R   K   K   R   I   V   T   G   N   P   R   C   Q   K   Y   F   L   K   E   I   P   I   Q   D    700

GTGGCCATTCAGGACTTCACTTGTGATGACGGAAATGATGACAATAGTTGCTCCCCACTTTCTCGCTGTCCTACT   2175
 V   A   I   Q   D   F   T   C   D   D   G   N   D   N   S   C   S   P   L   S   R   C   P   T    725

GAATGTACTTGCTTGGATACAGTCGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCCGAAAGGTATTCCAAGA   2250
 E   C   T   C   L   D   T   V   V   R   C   S   N   K   G   L   K   V   L   P   K   G   I   P   R    750

GATGTCACAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAACTCTCCAACTACAAACATTTA   2325
 D   V   T   E   L   Y   L   D   G   N   Q   F   T   L   V   P   K   E   L   S   N   Y   K   H   L    775

ACACTTATAGACTTAAGTAACAACAGAATAAGCACGCTTTCTAATCAGAGCTTCAGCAACATGACCCAGCTCCTC   2400
 T   L   I   D   L   S   N   N   R   I   S   T   L   S   N   Q   S   F   S   N   M   T   Q   L   L    800

ACCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCGCACCTTTGATGGATTAAAGTCTCTTCGATTA   2475
 T   L   I   L   S   Y   N   R   L   R   C   I   P   P   R   T   F   D   G   L   K   S   L   R   L    825

CTTTCTCTACATGGAAATGACATTTCTGTTGTGCCTGAAGGTGCTTTCAATGATCTTTCTGCATTATCACATCTA   2550
 L   S   L   H   G   N   D   I   S   V   V   P   E   G   A   F   N   D   L   S   A   L   S   H   L    850

GCAATTGGAGCCAACCCTCTTTACTGTGATTGTAACATGCAGTGGTTATCCGACTGGGTGAAGTCGGAATATAAG   2625
 A   I   G   A   N   P   L   Y   C   D   C   N   M   Q   W   L   S   D   W   V   K   S   E   Y   K    875

GAGCCTGGAATTGCTCGTTGTGCTGGTCCTGGAGAAATGGCAGATAAACTTTTACTCACAACTCCCTCCAAAAAA   2700
 E   P   G   I   A   R   C   A   G   P   G   E   M   A   D   K   L   L   L   T   T   P   S   K   K    900

TTTACCTGTCAAGGTCCTGTGGATGTCAATATTCTAGCTAAGTGTAACCCCTGCCTATCAAATCCGTGTAAAAAT   2775
 F   T   C   Q   G   P   V   D   V   N   I   L   A   K   C   N   P   C   L   S   N   P   C   K   N    925

GATGGCACATGTAATAGTGATCCAGTTGACTTTTACCGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGT   2850
 D   G   T   C   N   S   D   P   V   D   F   Y   R   C   T   C   P   Y   G   F   K   G   Q   D   C    950

GATGTCCCAATTCATGCCTGCATCAGTAACCCATGTAAACATGGAGGAACTTGCCACTTAAAGGAAGGAGAAGAA   2925
 D   V   P   I   H   A   C   I   S   N   P   C   K   H   G   G   T   C   H   L   K   E   G   E   E    975

GATGGATTCTGGTGTATTTGTGCTGATGGATTTGAAGGAGAAAATTGTGAAGTCAACGTTGATGATTGTGAAGAT   3000
 D   G   F   W   C   I   C   A   D   G   F   E   G   E   N   C   E   V   N   V   D   D   C   E   D   1000

AATGACTGTGAAAATAATTCTACATGTGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATACA   3075
 N   D   C   E   N   N   S   T   C   V   D   G   I   N   N   Y   T   C   L   C   P   P   E   Y   T   1025
```

```
GGTGAGTTGTGTGAGGAGAAGCTGGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAGTGCATC  3150
 G  E  L  C  E  E  K  L  D  F  C  A  Q  D  L  N  P  C  Q  H  D  S  K  C  I     1050

CTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCGATTTTGACGAC  3225
 L  T  P  K  G  F  K  C  D  C  T  P  G  Y  V  G  E  H  C  D  I  D  F  D  D     1075

TGCCAAGACAACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATACGTGCATATGCCCCGAA  3300
 C  Q  D  N  K  C  K  N  G  A  H  C  T  D  A  V  N  G  Y  T  C  I  C  P  E     1100

GGTTACAGTGGCTTGTTCTGTGAGTTTTCTCCACCCATGGTCCTCCCTCGTACCAGCCCCTGTGATAATTTTGAT  3375
 G  Y  S  G  L  F  C  E  F  S  P  P  M  V  L  P  R  T  S  P  C  D  N  F  D     1125

TGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTCAGTGTTTGCCTGGCTATCAGGGAGAA  3450
 C  Q  N  G  A  Q  C  I  V  R  I  N  E  P  I  C  Q  C  L  P  G  Y  Q  G  E     1150

AAGTGTGAAAAATTGGTTAGTGTGAATTTTATAAACAAAGAGTCTTATCTTCAGATTCCTTCAGCCAAGGTTCGG  2525
 K  C  E  K  L  V  S  V  N  F  I  N  K  E  S  Y  L  Q  I  P  S  A  K  V  R     1175

CCTCAGACGAACATAACACTTCAGATTGCCACAGATGAAGACAGCGGAATCCTCCTGTATAAGGGTGACAAAGAC  3600
 P  Q  T  N  I  T  L  Q  I  A  T  D  E  D  S  G  L  L  Y  K  G  D  K  D     1200

CATATCGCGGTAGAACTCTATCGGGGGCGTGTTCGTGCCAGCTATGACACCGGCTCTCATCCAGCTTCTGCCATT  3675
 H  I  A  V  E  L  Y  R  G  R  V  R  A  S  Y  D  T  G  S  H  P  A  S  A  I     1225

TACAGTGTGGAGACAATCAATGATGGAAACTTCCACATTGTGGAACTACTTGCCTTGGATCAGAGTCTCTCTTTG  3750
 Y  S  V  E  T  I  N  D  G  N  F  H  I  V  E  L  L  A  L  D  Q  S  L  S  L     1250

TCCGTGGATGGTGGGAACCCCAAAATCATCACTAACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTC  3825
 S  V  D  G  G  N  P  K  I  I  T  N  L  S  K  Q  S  T  L  N  F  D  S  P  L     1275

TATGTAGGAGGCATGCCAGGGAAGAGTAACGTGGCATCTCTGCGCCAGGCCCCTGGGCAGAACGGAACCAGCTTC  3900
 Y  V  G  G  M  P  G  K  S  N  V  A  S  L  R  Q  A  P  G  Q  N  G  T  S  F     1300

CACGGCTGCATCCGGAACCTTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATT  3975
 H  G  C  I  R  N  L  Y  I  N  S  E  L  Q  D  F  Q  K  V  P  M  Q  T  G  I     1325

TTGCCTGGCTGTGAGCCATGCCACAAGAAGGTGTGTGCCCATGGCACATGCCAGCCCAGCAGCCAGGCAGGCTTC  4050
 L  P  G  C  E  P  C  H  K  K  V  C  A  H  G  T  C  Q  P  S  S  Q  A  G  F     1350

ACCTGCGAGTGCCAGGAAGGATGGATGGGGCCCCTCTGTGACCAACGGACCAATGACCCTTGCCTTGGAAATAAA  4125
 T  C  E  C  Q  E  G  W  M  G  P  L  C  D  Q  R  T  N  D  P  C  L  G  N  K     1375

TGCGTACATGGCACCTGCTTGCCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGAGGTGTC  4200
 C  V  H  G  T  C  L  P  I  N  A  F  S  Y  S  C  K  C  L  E  G  H  G  G  V     1400

CTCTGTGATGAAGAGGAGGATCTGTTTAACCCATGCCAGGCGATCAAGTGCAAGCATGGGAAGTGCAGGCTTTCA  4275
 L  C  D  E  E  E  D  L  F  N  P  C  Q  A  I  K  C  K  H  G  K  C  R  L  S     1425

GGTCTGGGGCAGCCCTACTGTGAATGCAGCAGTGGATACACGGGGGACAGCTGTGATCGAGAAATCTCTTGTCGA  4350
 G  L  G  Q  P  Y  C  E  C  S  S  G  Y  T  G  D  S  C  D  R  E  I  S  C  R     1450

GGGGAAAGGATAAGAGATTATTACCAAAAGCAGCAGGGCTATGCTGCTTGCCAAACAACCAAGAAGGTGTCCCGA  4425
 G  E  R  I  R  D  Y  Y  Q  K  Q  Q  G  Y  A  A  C  Q  T  T  K  K  V  S  R     1475

TTAGAGTGCAGAGGTGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGAGGAGCAAGCGGCGGAAATACTCTTTC  4500
 L  E  C  R  G  G  C  A  G  G  Q  C  C  G  P  L  R  S  K  R  R  K  Y  S  F     1500

GAATGCACTGACGGCTCCTCCTTTGTGGACGAGGTTGAGAAAGTGGTGAAGTGCGGCTGTACGAGGTGTGTGTCC  4575
 E  C  T  D  G  S  S  F  V  D  E  V  E  K  V  V  K  C  G  C  T  R  C  V  S     1525
```